



OIPE

RAW SEQUENCE LISTING

DATE: 01/26/2002

PATENT APPLICATION: US/09/877,160

TIME: 15:58:15

Input Set : A:\12774-003001.TXT

Output Set: N:\CRF3\01262002\I877160.raw

ENTERED

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4 <110> APPLICANT: Ching-Hsaing, Hsu
5      Cheng, Winston T. K.
7 <120> TITLE OF INVENTION: ALLERGEN-CONTAINING MILK FOR ALLERGY
8      TREATMENT
10 <130> FILE REFERENCE: 12774-003001
12 <140> CURRENT APPLICATION NUMBER: 09/877,160
13 <141> CURRENT FILING DATE: 2001-06-08
15 <160> NUMBER OF SEQ ID NOS: 10
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 132
21 <212> TYPE: PRT
22 <213> ORGANISM: Dermatophagoides pteronyssinus
24 <400> SEQUENCE: 1
25 Met Lys Phe Ile Ile Ala Phe Phe Val Ala Thr Leu Ala Val Met Thr
26 1          5          10          15
27 Val Ser Gly Glu Asp Lys Lys His Asp Tyr Gln Asn Glu Phe Asp Phe
28 20          25          30
29 Leu Leu Met Glu Arg Ile His Glu Gln Ile Lys Lys Gly Glu Leu Ala
30 35          40          45
31 Leu Phe Tyr Leu Gln Glu Gln Ile Asn His Phe Glu Glu Lys Pro Thr
32 50          55          60
33 Lys Glu Met Lys Asp Lys Ile Val Ala Glu Met Asp Thr Ile Ile Ala
34 65          70          75          80
35 Met Ile Asp Gly Val Arg Gly Val Leu Asp Arg Leu Met Gln Arg Lys
36 85          90          95
37 Asp Leu Asp Ile Phe Glu Gln Tyr Asn Leu Glu Met Leu Lys Lys Ser
38 100         105         110
39 Gly Asp Ile Leu Glu Arg Asp Leu Lys Lys Glu Glu Ala Arg Val Lys
40 115         120         125
41 Asn Ile Glu Val
42 130
44 <210> SEQ ID NO: 2
45 <211> LENGTH: 320
46 <212> TYPE: PRT
47 <213> ORGANISM: Dermatophagoides pteronyssinus
49 <400> SEQUENCE: 2
50 Met Lys Ile Val Leu Ala Ile Ala Ser Leu Leu Ala Leu Ser Ala Val
51 1          5          10          15
52 Tyr Ala Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala
53 20          25          30
54 Phe Asn Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys
55 35          40          45

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56 Asn Phe Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile
57      50                      55                      60
58 Asn His Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu
59 65                      70                      75                      80
60 Met Ser Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn
61                      85                      90                      95
62 Ala Glu Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile
63                      100                      105                      110
64 Asp Leu Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly
65                      115                      120                      125
66 Cys Gly Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala
67      130                      135                      140
68 Tyr Leu Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu
69 145                      150                      155                      160
70 Val Asp Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg
71                      165                      170                      175
72 Gly Ile Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr
73                      180                      185                      190
74 Arg Tyr Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg
75                      195                      200                      205
76 Phe Gly Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys
77      210                      215                      220
78 Ile Arg Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile
79 225                      230                      235                      240
80 Gly Ile Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile
81                      245                      250                      255
82 Ile Gln Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile
83                      260                      265                      270
84 Val Gly Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn
85                      275                      280                      285
86 Ser Trp Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala
87      290                      295                      300
88 Asn Ile Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
89 305                      310                      315                      320
91 <210> SEQ ID NO: 3
92 <211> LENGTH: 146
93 <212> TYPE PRT
94 <213> ORGANISM: Dermatophagoides pteronyssinus
96 <400> SEQUENCE: 3
97 Met Met Tyr Lys Ile Leu Cys Leu Ser Leu Leu Val Ala Ala Val Ala
98 1      5                      10                      15
99 Arg Asp Gln Val Asp Val Lys Asp Cys Ala Asn His Glu Ile Lys Lys
100                      20                      25                      30
101 Val Leu Val Pro Gly Cys His Gly Ser Glu Pro Cys Ile Ile His Arg
102                      35                      40                      45
103 Gly Lys Pro Phe Gln Leu Glu Ala Val Phe Glu Ala Asn Gln Asn Thr
104      50                      55                      60
105 Lys Thr Ala Lys Ile Glu Ile Lys Ala Ser Ile Asp Gly Leu Glu Val
106 65                      70                      75                      80

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107 Asp Val Pro Gly Ile Asp Pro Asn Ala Cys His Tyr Met Lys Cys Pro
108                               85                               90                               95
109 Leu Val Lys Gly Gln Gln Tyr Asp Ile Lys Tyr Thr Trp Asn Val Pro
110                               100                              105                              110
111 Lys Ile Ala Pro Lys Ser Glu Asn Val Val Val Thr Val Lys Val Met
112                               115                              120                              125
113 Gly Asp Asp Gly Val Leu Ala Cys Ala Ile Ala Thr His Ala Lys Ile
114                               130                              135                              140
115 Arg Asp
116 145
118 <210> SEQ ID NO: 4
119 <211> LENGTH: 21
120 <212> TYPE: DNA
121 <213> ORGANISM: Artificial Sequence
123 <220> FEATURE:
124 <223> OTHER INFORMATION: oligonucleotide for PCR
126 <400> SEQUENCE: 4
127 tcgcgtagaa tcgattcatg t                                     21
129 <210> SEQ ID NO: 5
130 <211> LENGTH: 21
131 <212> TYPE: DNA
132 <213> ORGANISM: Artificial Sequence
134 <220> FEATURE:
135 <223> OTHER INFORMATION: oligonucleotide for PCR
137 <400> SEQUENCE: 5
138 tacgcgtagc ctgggtggca t                                     21
140 <210> SEQ ID NO: 6
141 <211> LENGTH: 20
142 <212> TYPE: DNA
143 <213> ORGANISM: Artificial Sequence
145 <220> FEATURE:
146 <223> OTHER INFORMATION: oligonucleotide for PCR
148 <400> SEQUENCE: 6
149 gctcgagcat gaaattcatc                                     20
151 <210> SEQ ID NO: 7
152 <211> LENGTH: 23
153 <212> TYPE: DNA
154 <213> ORGANISM: Artificial Sequence
156 <220> FEATURE:
157 <223> OTHER INFORMATION: oligonucleotide for PCR
159 <400> SEQUENCE: 7
160 actcgagtga tgaaggcaac aag                                     23
162 <210> SEQ ID NO: 8
163 <211> LENGTH: 20
164 <212> TYPE: DNA
165 <213> ORGANISM: Artificial Sequence
167 <220> FEATURE:
168 <223> OTHER INFORMATION: oligonucleotide for PCR
170 <400> SEQUENCE: 8

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171 ctctcttctgct atcctcttcc                                20
173 <210> SEQ ID NO: 9
174 <211> LENGTH: 23
175 <212> TYPE: DNA
176 <213> ORGANISM: Artificial Sequence
178 <220> FEATURE
179 <223> OTHER INFORMATION: oligonucleotide for PCR
181 <400> SEQUENCE 9
182 actcagagtga tgaaggcaag aag                                23
184 <210> SEQ ID NO: 10
185 <211> LENGTH: 624
186 <212> TYPE: DNA
187 <213> ORGANISM: Dermatophagoides pteronyssinus
189 <220> FEATURE
190 <221> NAME/KEY: CDS
191 <222> LOCATION (62)...(457)
193 <400> SEQUENCE 10
194 gtgaccccat ttcagaatct tgaaggctaa ccatactag tgaattcgcg gccgctcgag    60
195 c atg aaa ttc atc att gct ttc ttt gtt gcc act ttg gca gtt atg act    109
196 Met Lys Phe Ile Ile Ala Phe Phe Val Ala Thr Leu Ala Val Met Thr
197 1 5 10 15
199 gtt tca ggt gaa gat aaa aaa cat gat tat caa aat gaa ttt gat ttc    157
200 Val Ser Gly Glu Asp Lys Lys His Asp Tyr Gln Asn Glu Phe Asp Phe
201 20 25 30
203 tta ttg atg gaa cgt att cat gaa caa att aaa aaa ggt gaa ctt gca    205
204 Leu Leu Met Glu Arg Ile His Glu Gln Ile Lys Lys Gly Glu Leu Ala
205 35 40 45
207 ttg ttc tat ctt caa gaa cag att aat cat ttt gaa gaa aaa cca aca    253
208 Leu Phe Tyr Leu Gln Glu Gln Ile Asn His Phe Glu Glu Lys Pro Thr
209 50 55 60
211 aaa gaa atg aaa gat aaa att gta gcc gaa atg gat acc att att gct    301
212 Lys Glu Met Lys Asp Lys Ile Val Ala Glu Met Asp Thr Ile Ile Ala
213 65 70 75 80
215 atg atc gat ggt gta cgt ggt gta ctt gat cgt ctt atg caa cgt aaa    349
216 Met Ile Asp Gly Val Arg Gly Val Leu Asp Arg Leu Met Gln Arg Lys
217 85 90 95
219 gat tta gat att ttt gaa caa tat aat ctt gaa atg ctc aaa aaa tct    397
220 Asp Leu Asp Ile Phe Glu Gln Tyr Asn Leu Glu Met Leu Lys Lys Ser
221 100 105 110
223 ggt gat att ttg gaa cgt gat ttg aaa aaa gaa gaa gca cgt gtt aaa    445
224 Gly Asp Ile Leu Glu Arg Asp Leu Lys Lys Glu Glu Ala Arg Val Lys
225 115 120 125
227 aat att gaa gtt aagctttgaa ttcagatcgg ttaccaacta cctagactgg    497
228 Asn Ile Glu Val
229 130
231 attcgtgaca atatgcggcc gtgatatcta cgtatgatca gccctcgactg tgccttcttg    557
232 ttgccttcac cactcgagtc tagagggccccc gtttaaaccg gctgatcagc ctcgactgtg    617
233 ccttcta                                                    624

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/877,160

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